AMENDMENTS TO THE SPECIFICATION

Please make the following amendments to the specification.

Please add the following section heading and paragraph after paragraph 0036 and before the section heading "BRIEF DESCRIPTION OF DRAWINGS":

BRIEF DESCRIPTION OF SEQUENCE LISTING APPENDIX

Reference is made to the appendix submitted herein. The appendix contains the following: Sequence_001.txt (25,165,878 kb); Sequence_002.txt (25,165,824 kb); Sequence_003.txt (25,165,824 kb); Sequence_004.txt (25,165,824 kb); Sequence_005.txt (25,165,824 kb); Sequence_006.txt (25,165,824 kb); Sequence_007.txt (25,165,824 kb); Sequence_008.txt (25,165,824 kb); Sequence_009.txt (25,165,824 kb); Sequence_010.txt (25,165,824 kb); Sequence_011.txt (25,165,824 kb); Sequence_012.txt (25,165,824 kb); Sequence_013.txt (25,165,824 kb); Sequence_014.txt (25,165,824 kb); Sequence_015.txt (25,165,824 kb); Sequence_016.txt (25,165,824 kb); Sequence_017.txt (25,165,824 kb); Sequence_018.txt (25,165,824 kb); Sequence_019.txt (25,165,824 kb); Sequence_020.txt (25,165,824 kb); Sequence_021.txt (25,165,824 kb); Sequence_022.txt (25,165,824 kb); Sequence_023.txt (25,165,824 kb); Sequence_024.txt (25,165,824 kb); Sequence_025.txt (25,165,824 kb); and Sequence_026.txt (8,761,241 kb), all of which were created on January 1, 2006, which together are a sequence listing in accordance with 37 C.F.R. §§ 1.821-1.825, the contents of which are incorporated by reference herein.

Please replace paragraph 0181 with the following paragraph:

Fig. 14B is a schematic representation of secondary folding of hairpins of the operon-like cluster of Fig. 14A. The hairpins shown are as follows: N2 (SEQ ID NO: 4205040), N3 (SEQ ID NO: 4205041), MIR23 (SEQ ID NO: 4205042), GAM22 (SEQ ID NO: 4205043), GAM7617 (SEQ ID NO: 4205044), N252 (SEQ ID NO: 4205045), N4 (SEQ ID NO: 4205046), N0 (SEQ ID NO: 4205047), N6 (SEQ ID NO: 4205048), MIR24 (SEQ ID NO: 4205049), and N7 (SEQ ID NO: 4205050).

Please replace paragraph 0183 with the following paragraph:

Fig. 15A is an annotated sequence of EST72223 (SEQ ID

NO: 4205035) comprising known human microRNA oligonucleotide MIR98 and novel human oligonucleotide GAM25 PRECURSOR detected by the oligonucleotide detection system of the present invention~~; and~~. Additionally annotated in EST72223 are the miRNA-98 hairpin in bold (SEQ ID NO: 4205036), the sequence of the mature miRNA-98 in bold and underline (SEQ ID NO: 4205037), the sequence of the GAM25 hairpin in bold (SEQ ID NO: 4205038), and the sequence of the mature miRNA of GAM25 in bold and underline (SEQ ID NO: 4205039).

Please replace paragraph 0192 with the following paragraph:

Fig. 19 presents pictures of laboratory results demonstrating laboratory confirmation of "dicing" of four novel bioinformatically-detected HIV1 GAM PRECURSORSs into their corresponding mature GAM RNAs[[;]]. Fig. 19A shows the sequence of HIV (U5-R) (SEQ ID NO: 4205083). Annotated in SEQ ID NO: 4205083 are: nucleotides 1-57 (SEQ ID NO: 4205084) in bold; the bold, underlined sequence of nucleotides 2-23 (SEQ ID NO: 4205085); the bold sequence of nucleotides 30-77 (SEQ ID NO: 4205086); and the bold, underlined sequence of nucleotides 60-77 (SEQ ID NO: 4205087). Fig. 19B shows an HIV TRANSCRIPT SEQUENCE (SEQ ID NO: 4205088). Annotated in SEQ ID NO: 4205088 is the underlined sequence of nucleotides 42-65 (SEQ ID NO: 4205089). Also shown in Fig. 19D is a sequence named "GAM RNA" (SEQ ID NO: 4205090). Fig. 19E shows an HIV TRANSCRIPT SEQUENCE (SEQ ID NO: 4205091). Annotated in SEQ ID NO: 4205091 is the underlined sequence of nucleotides 102-125 (SEQ ID NO: 4205092). Also shown in Fig. 19E is a sequence named "GAM RNA" (SEQ ID NO: 4205093).

Please replace paragraph 0345 with the following paragraph:

The sequence presented in Row 29 is a representative of the group of five GAM RNAs. The full list of GAM RNA sequences and their corresponding precursors is as follows (each GAM RNA sequence is followed by the GAM Name): TCACTGCAACCTCC ACCTCCCA (352092, 352651,355761) (SEQ ID NO. 4204916), TCACTGCAACCTCCACCTCCCG (351868, 352440, 351973, 352169, 352445, 358164, 353737, 352382, 352235, 352232, 352268, 351919, 352473, 352444, 353638, 353004, 352925, 352943) (SEQ ID NO: 4204917), TCACTGCAACCTCCACCTC CTG (358311) (SEQ ID NO: 4204918), TCACTGCA |ACCTCCACCTTCAG (353323) (SEQ ID NO: 4204919), and TCACTGCAACCTCCACCTTCCG (353856) (SEQ ID NO:

4204920).

Please replace paragraphs 0360-0362 with the following paragraphs:

Two types of cDNA libraries, designated "One-tailed" and "Ligation", were prepared from the one of the abovementioned fractionated RNA samples. RNA was dephosphorylated and ligated to an RNA (designated with lowercase letters)-DNA (designated with UPPERCASE letters) hybrid 5'-phosphorylated, 3'idT blocked 3'-adapter (5'-P-uuuAACCGCATCCTTCTC-idT-3' (SEQ ID NO: 4204921), Dharmacon #P-002045-01-05) (as elaborated in Elbashir et al., Genes Dev.15:188-200 (2001)) resulting in ligation only of RNase III type cleavage products.3'-Ligated RNA was excised and purified from a half 6%,half 13% polyacrylamide gel to remove excess adapter with a Nanosep 0.2 microM centrifugal device (Pall) according to instructions, and precipitated with glycogen and 3 volumes of ethanol. Pellet was resuspended in a minimal volume of water.

For the "Ligation" library, a DNA (UPPERCASE)-RNA (lowercase) hybrid 5'-adapter (5'-TACTAATACGACTCACTaaa-3' (SEQ ID NO: 4204922) Dharmacon #P-002046-01-05) was ligated to the 3'-adapted RNA, reverse transcribed with "EcoRI-RT": (5'-GACTAGCTGGAATTCAAGGATGCGGTTAAA-3') (SEQ ID NO: 4204923), PCR-amplified with two external primers essentially as in Elbashir et al. (2001), except that primers were "EcoRI-RT" and "PstI Fwd" (5'-CAGCCAACGCTGCAGATA CGACTCACTAAA-3') (SEQ ID NO: 4204924). This PCR product was used as a template for a second round of PCR with one hemispecific and one external primer or with two hemispecific primers.

For the "One-tailed" library, the 3'-adapted RNA was annealed to 20pmol primer "EcoRI RT" by heating to 70 C and cooling 0.1 C/sec to 30 C and then reverse-transcribed with Superscript II RT (according to manufacturer's instructions, Invitrogen) in a 20 microliters volume for 10 alternating 5 minute cycles of 37 C and 45 C. Subsequently, RNA was digested with 1 microliter 2M NaOH and 2mM EDTA at 65 C for 10 minutes. cDNA was loaded on a polyacrylamide gel, excised and gel-purified from excess primer as above (invisible, judged by primer run alongside) and resuspended in 13 microliters of water. Purified cDNA was then oligo-dC tailed with 400U of recombinant terminal transferase (Roche Molecular Biochemicals), 1 microliter 100 microM dCTP, 1 microliter 15mM $CoCl_2$, and 4 microliters reaction buffer, to a final volume of 20 microliters for 15 minutes at 37 C. Reaction was stopped with 2 microliters 0.2M EDTA and 15 microliters 3M

NaOAc pH 5.2.Volume was adjusted to 150 microliters with water, Phenol:Bromochloropropane 10:1 extracted and subsequently precipitated with glycogen and 3 volumes of ethanol. C-tailed cDNA was used as a template for PCR with the external primers "T3-PstBsg(G/I)18" (5'-AATTAACCCTCACTAAAGGCTGCA GGTGCAGGIGGGIIGGGIIGGGIIGN-3' (SEQ ID NO: 4204925) where I stands for Inosine and N for any of the 4 possible deoxynucleotides), and with "EcoRI Nested" (5'-GGAATTCA AGGATGCGGTTA-3') (SEQ ID NO: 4204926). This PCR product was used as a template for a second round of PCR with one hemispecific and one external primer or with two hemispecific primers.

Please replace paragraph 0364 with the following paragraph:

Hemispecific primers were constructed for each predicted GAM RNA oligonucleotide by an in-house program designed to choose about half of the 5'or 3'sequence of the GAM RNA corresponding to a TM of about 30 -34 C constrained by an optimized 3'clamp,appended to the cloning adapter sequence (for "One-tailed" libraries, 5'-GGNNGGGNNG (SEQ ID NO: 4204927) on the 5'end or TTTAACCGCATC-3' (SEQ ID NO: 4204947) on the 3' end of the GAM RNA; for "Ligation" libraries, the same 3' adapter and 5'-CGACTCACTAAA (SEQ ID NO: 4204928) on the 5' end of the GAM RNA). Consequently, a fully complementary primer of a TM higher than 60 C was created covering only one half of the GAM RNA sequence permitting the unbiased elucidation by sequencing of the other half.

Please replace paragraph 0389 with the following paragraph:

Transcript products were 705 nt (EST72223),102 nt (MIR98 precursor), 125 nt (GAM25 precursor) long.EST72223 was PCR-amplified with T7-EST 72223 forward primer: 5'-TAATACG ACTCACTATAGGCCCTTATTAGAGGATTCTGCT-3' (SEQ ID NO: 4204929) and T3-EST72223 reverse primer: 5"-AATTAACCCTCACTAAAGGTTTTTTTTTCCTGAGACAGAG T-3'. (SEQ ID NO: 4204930). MIR98 was PCR-amplified using EST72223 as a template with T7MIR98 forward primer: 5'-TAAT ACGACTCACTATAGGGTGAGGTAGTAAGTTGTATTGTT-3' (SEQ ID NO: 4204931) and T3MIR98 reverse primer: 5'-AAT TAACCCTCACTAAAGGGAAAGTAGTAAGTTGTATAGTT-3' (SEQ ID NO: 4204932). GAM25 was PCR-amplified using EST72223 as a template with GAM25 forward primer: 5'-GA GGCAGGAGAATTGCTTGA-3' (SEQ ID NO: 4204933) and T3-EST72223 reverse primer: 5'-AATTAACCCTCACTAAAGG

CCTGAGACAGAGTCTTGCTC-3' (SEQ ID NO: 4204934).

Please replace paragraph 0392 with the following paragraph:

Reference is now made to Fig.16A, which depicts a first method that uses primers designed to the stems of the hairpins.Since the stem of the hairpins often has bulges, mismatches, as well as G-T pairing,which is less significant in DNA than is G-U pairing in the original RNA hairpin, the primer pairs were engineered to have the lowest possible match to the other strand of the stem. Thus, the F-Stem primer, derived from the 5'stem region of the hairpin, was chosen to have minimal match to the 3'stem region of the same hairpin. Similarly, the R-stem primer, derived from the 3'region of the hairpin (reverse complementary to its sequence),was chosen to have minimal match to the 5'stem region of the same hairpin. The F-Stem primer was extended in its 5'sequence with the T3 primer (5'-ATTAACCCTCACTAAAGGGA-3' (SEQ ID NO: 4204935)) and the R-Stem primer was extended in its 5' sequence with the T7 primer (5'-TAATACGACTCACTATAGGG (SEQ ID NO: 4204936). The extension is needed to obtain a large enough fragment for direct sequencing of the PCR product. Sequence data from the amplified hairpins is obtained in two ways. One way is the direct sequencing of the PCR products using the T3 primer that matches the extension of the F-Stem primer. Another way is the cloning of the PCR products into a plasmid, followed by PCR screening of individual bacterial colonies using a primer specific to the plasmid vector and either the R-Loop (Fig.16B) or the F-Loop (Fig.16C) primer. Positive PCR products are then sent for direct sequencing using the vector-specific primer.

Please replace paragraphs 0453-0473 with the following paragraphs:

Sequence:5'(5phos)rUrGrGCCTATAGTGAGTCGTATTA(3Invd T)3' (SEQ ID NO: 4204937)

2.Name:5Ada RNA-DNA XbaBseRI

Sequence:5'AAAGGAGGAGCTCTAGrArUrA 3' (SEQ ID NO: 4204938). or optionally:

3.Name:5Ada MC RNA-DNA PstAtaBser

Sequence:5'CCTAGGAGGAGGACGTCTGrCrArG 3' (SEQ ID NO: 4204939).

4.Name:3'Ada nT7 MC RNA-DNA

Sequence:5'(5phos)rCrCrUATAGTGAGTCGTATTATCT (3InvdT)3' (SEQ ID NO: 4204940).

The following DNA primers are included in the present invention:

1.Name:T7 NcoI-RT-PCR primer

Sequence:5'TAATACGACTCACTATAGGCCA 3' (SEQ ID NO: 4204941).

2.Name:T7NheI SpeI-RT-PCR primer

Sequence:5'GCTAGCACTAGTTAATACGACTCACTATAGGC CA 3' (SEQ ID NO: 4204942).

3.Name:5Ada XbaBseRI Fwd

Sequence:5'AAAGGAGGAGCTCTAGATA 3' (SEQ ID NO: 4204943).

4.Name:Pst-5Ada XbaBseRI Fwd

Sequence:5'TGACCTGCAGAAAGGAGGAGCTCTAGATA 3' (SEQ ID NO: 4204944).

or optionally:

5.Name:5Ada MC PstAtaBser fwd

Sequence:5'ATCCTAGGAGGAGGACGTCTGCAG 3' (SEQ ID NO: 4204945).

6.Name:RT nT7 MC XbaI

Sequence:5'GCTCTAGGATAATACGACTCACTATAGG 3' (SEQ ID NO: 4204946).